On page 68, line 10, change "(SEQ ID NO: 49)" to --(SEQ ID NO. 56)--.

On page 70, line 4, change "(SEQ ID NO: 50)" to --(SEQ ID NO. 57)--.

On page 70, line 5, change "(SEQ ID NO: 51)" to --(SEQ ID NO. 58)--.

On page 70, line 6, after "AT # 909" add --(SEQ ID NO. 59)--.

On page 70, line 6, after "ribosomal protein L19" add --(SEQ ID NO:60)--.

In the Claims

Cancel Claims 1 - 44.

45. (Amended) A method of compiling a positive sense functional gene profile of an organism comprising:

(a) preparing a [vector library of DNA or RNA sequences] library of cDNAs, genomic DNAs, or a pool of RNAs from a non-plant donor organism, [each sequence being in a positive sense orientation] and constructing recombinant viral nucleic acids comprising a nucleic acid insert derived from said library;

(b) infecting a plant host with [a vector] one of said recombinant viral nucleic acids;

(c) transiently expressing the [donor DNA or RNA sequence] nucleic acid in a positive sense orientation in said [growing] plant host;

(d) determining one or more phenotypic or biochemical changes in said plant host;

(e) identifying [an associated trait where] a trait associated with a phenotypic or biochemical change [occurs];

(f) identifying a donor gene [associated with the trait;] or

[(g) identifying] a plant host gene, which is associated with the trait; and

(g) repeating steps b) – [g] f) until at least one donor organism gene or one plant host gene associated with said trait is identified, whereby a positive sense functional gene profile of said plant host [and] or [of] said donor organism is compiled.

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--46.   (New) The method according to Claim 45, wherein said plant host is *Nicotiana.*

47.   (New) The method according to Claim 46, wherein said plant host is *Nicotiana benthamina* or *Nicotiana cleavlandii.*

48.   (New) The method according to Claim 45, wherein said recombinant viral nucleic acids further comprise a native plant viral subgenomic promoter and a plant viral coat protein coding sequence.

49.   (New) The method according to Claim 48, wherein said recombinant viral nucleic acids further comprise a non-native plant viral subgenomic promoter, said native plant viral subgenomic promoter initiates transcription of said plant viral coat protein sequence and said non-native plant viral subgenomic promoter initiates transcription of said nucleic acid insert sequence.

50.   (New) The method according to Claim 45, wherein a plus sense RNA is produced in the cytoplasm of said host plant, and said plus sense RNA results in an overexpression of a protein in said host plant.

51.   (New) The method according to Claim 45, wherein a plus sense RNA is produced in the cytoplasm of said host plant, and said plus sense RNA results in an enhanced or reduced expression of an endogenous gene in said plant host.

52.   (New) The method according to Claim 45, wherein said nucleic acid insert sequence encodes a GTP binding protein.

53.   (New) The method according to Claim 45, wherein said plus sense RNA results in a reduced expression of an endogenous gene in said plant host.

54.   (New) The method according to Claim 45, wherein said recombinant viral nucleic acids are derived from a plant virus.

55.   (New) The method according to Claim 54, wherein said plant virus is selected